CLAIMS

1. A method of defining the differentiation grade of tumor with genes and/or proteins selected by the statistical analyses based on the expression level or pattern of the genes and/or proteins of human tumor tissues obtainable from cancer patients.

2. A method according to claim 1, wherein the human tissues are human liver tissues.

3. A method according to claim 2, wherein the differentiation grade of tumor is selected from the group consisting of non-cancerous liver, pre-cancerous liver, well differentiated hepatocellular carcinoma (HCC), moderately differentiated HCC, and poorly differentiated HCC.

4. A method according to claim 3, wherein the genes and/or proteins are differentially expressed between non-cancerous liver and pre-cancerous liver, pre-cancerous liver and well differentiated hepatocellular carcinoma (HCC), well differentiated HCC and moderately differentiated HCC, or moderately differentiated HCC and poorly differentiated HCC.

5. A method according to any one of claims 1 to 4, wherein the expression level or pattern of genes and/or proteins is examined by means of DNA microarray, reverse transcription polymerase-chain reaction or protein array.

6. A method according to claim 5, wherein the genes and/or proteins are selected in descending order of the Fisher ratio.

7. A method according to claim 5 or 6, wherein the number of the genes and/or proteins is between 40 and 100.

8. A method according to claim 5 or 6, wherein the number of the genes and/or proteins is between 35 and 45.

9. A method according to claim 8, wherein the number of the genes and/or proteins is 40.

10. A method of defining the differentiation grade of tumor, the method comprising steps of:

(a) selecting genes and/or proteins that have the highest Fisher ratios in comparison between non-cancerous liver and pre-cancerous liver, pre-cancerous liver and well differentiated hepatocellular carcinoma (HCC), well differentiated HCC and moderately differentiated HCC, or moderately differentiated HCC and poorly differentiated HCC; and

(b) defining the differentiation grade of tumor by using the genes and/or proteins.

11. A method of defining the differentiation grade of tumor, the method comprising steps of:

(a) determining the number of genes and/or proteins to define the differentiation grade of tumor;

(b) selecting a number of genes and/or proteins decided in step (a) that have the highest Fisher ratios in comparison between non-cancerous liver and pre-cancerous liver, pre-cancerous liver and well differentiated hepatocellular carcinoma (HCC), well differentiated HCC and moderately differentiated HCC, or moderately differentiated HCC and poorly differentiated HCC;

(c) applying the data of genes and/or proteins selected in step (b) to all samples; and

(d) defining the differentiation grade of tumor.

12. A method of defining the differentiation grade of tumor, the method comprising steps of:

(a) determining the number of genes and/or proteins to define the differentiation grade of tumor;

(b) selecting a number of genes and/or proteins decided in step (a) that have the highest Fisher ratios in comparison between non-cancerous liver and pre-cancerous liver, pre-cancerous liver and well differentiated hepatocellular carcinoma (HCC), well differentiated HCC and moderately differentiated HCC, or moderately differentiated HCC and poorly differentiated HCC;

(c) applying the data of genes and/or proteins selected in step (b) to all samples;

(d) designing a minimum distance classifier with the data of genes and/or proteins selected in step (b);

(e) applying the minimum distance classifier designed in step (d) to all samples;

(f) generating self-organizing map with the data of all the genes and/or proteins selected in step (b);

(g) applying the self organizing map generated in step (f) to all samples; and

(h) defining the differentiation grade of tumor.

13. A kit for carrying out the method according to any one of claims 1 to 12, the kit comprises DNA chips, oligonucleotide chips, protein chips, probes or primers that are necessary for effecting DNA microarrays, oligonucleotide microarrays, protein arrays, northern blotting, RNase protection assays, western blotting, and reverse transcription polymerase-chain reaction to examine the expression of the genes and/or proteins selected by the statistical analyses in claims 1 to 12.

14. Use of genes and/or proteins according to any one of claims 1 to 12 for screening anti-cancer agents.

15. Use of antibodies specific to genes and/or proteins according to any one of claims 1 to 12 for treating tumors in different grades.